

Inventor: ANDREASSON et al.
Docket No.: 09663.0068USWO
Title: PLANT DISEASE RESISTANCE AND SAR REGULATOR PROTEIN
Attorney Name: Denise M. Kettelberger
Phone No.: 612.371.5268
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Figure 1 A.

		BD fusion	AD fusion	-His growth	-Leu growth	β -gal activity	-Ade-Trp growth
MPK4	MKS1			+	+	+	+
MKS1	MPK4			+	+	+	+
MKS1	MPK3			-	-	-	+
MKS1	MPK5			-	-	-	+
MKS1	MPK6			-	-	-	+
MKS1	MPK17			-	-	-	+
MKS1	WRKY25			+	+	+	+
MKS1	WRKY33			+	+	+	+
MKS1	WRKY26			-	-	-	+
MKS1	WRKY29			-	-	-	+
MPK4	WRKY25			-	-	-	+
MPK4	WRKY33			-	-	-	+

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Figure 1B (1)

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1 MSSTSSPPPPSK-----AKRRGCTHCAREOPLIVSSAPAEASPSKKPRVS-----GGG
1 MSSTSSPPPPSK-----AKRRGCTHCAREOPLIVSSAPAEASPSKKPRVS-----GGG
1 MTMTVATMPSSDASSPPPKRPTATGGGLGPRPLPLKVLSSPSSSSSSSSSSPAS-NKP-----PASTT
1 MTMTVAMPSSS-----SSRRGGLRGPRPLPLKVLSSSRRGSSPSSSSASKG-----ASKK
1 -----SLOGPRPLPLIIPPGSGTSSSSSSSTPRPA-KRPRRVSSGGGDVSRAPQSSA
1 -----MDPSEYFAGGNPSDQONQKQLOLCGPRPSPLSVNKHSHKIKKPP-----KHPAPPP-NRDQPPPY
1 -----MDPSESFAGGNPSDQONQKQLOLCGPRPSPLSVNKHSHKIKKPP-----KHPAPPPQ-HRDQAPLY
1 -----MDPSEHFAGGNPFDDQTPKQLOLCGPRPSPLSVNKHSHKIKKPP-----RHPAPPPQHHRDQAPLY
1 -----QLOGPRPLPLIIPPGSGTSSSSSSSTPRPA-KRPRRVSSGGGDVSRAPQSSA
1 -----MDNRSPSRGILGPRPLPLKVLGDSHKTIRKPPPLAPP-----PQPQPPQTHQQEFSQSR
1 MEFPSSSTSPSPSSSGQHQQQPTTFRRLCGPRPRLNVRMESHATKKPSGAAAA--AAQAQAHQLPAQAARREQQQP
1 MDPPSSSG-----RPTTFRRLCGPRPRLNVRMESHATKKPS-----ASGAPPAPGQGRPRDHHHHHPQ
1 -----QGRPRPLAVSKDSHKVRLPVAPQRQHQHQQPAQLQQQHQYHQQQQQ
1 -----MDQSSSTLNLNQ-----RKSSSSPTTRTPPKOK-----RKSTT
1 -----MESSSSSTFTTTSLDKKPSPVSRKSPKOK-----KKTTS
1 -----MVRNSMKAEDIDHLPQTFYGDYSKTLVPLNKNNS-----QIITK
1 -----METQYQSFH-EGSSSRVSMNNS-----QVISK
1 -----MEATIFEKRSSLSSTAVKOS-----YSITK
1 -----METBATTVOKRRS-LPTTAMHKOS-----RTLTK
1 -----MEQQLSSPASQSGGGRGCGPRPAPLVKRNESHKIRKOE-----PVQ
1 -----MLPTRCNEINGSRPSSSLTAGESTTKTSCKSKP-----RPF
1 -----MPSRSSMASPLLQRPDLGPRPAPLVSTGTTTGTADLQLQVNN-----RR
1 -----MDRQSQSSRENATATRGGGSSGSGGGGGVG-----KAA
1 -----MAAASFDAADVTRCGTGRALGVHAASHKIKKPPPGAG-----HQQ
1 -----MSKKAKN-----
1 -----NFKDVIQRLTCKPFDNKQPAKAGEVSPAER-----LAI
      r      i      gprp      l      v      dsh      ikk      tk
      DOMAIN 1

1 C3 DELETION
51 GDTGPVILYEL-PRVHVEQEEMAVVOKLTGG-----KQOPAAASTLTTL
51 GDTGPVILYEL-PRVHVEQEEMAVVOKLTGG-----KQOPAAASTLTTL
66 AKRPPVILYELTPRVHVEQEEMAVVOKLTGG-----KHPRAAPTSS--
50 SAAAPVILYELTPRVHVEQEEMAVVOKLTGG-----KPPAPPPVMMFA
53 AAPGPVILYELTPRVHVEQEEMAVVOKLTGG-----RRGQGAVER--
61 IPREPVIYAVSPKVIHATASEFMNVORLTGSSGV-----FLESGGGDVSPAAR
62 AAREPVIYAVSPKVIHTTASEFMNVORLTGSSAV-----FLESGGGDVSPAAR
63 PPREPVIYAVSPKVIHTTASEFMNVORLTGSSSEV-----FLESRNDGDVSPAAR
35 PPROPIIYITVSPKVIHTTASEFMNVORLTGSSSSS-----SAEVVMSNNNN--
56 PPGPVIYITVSPRIIHTHFNFMNLVORLTGKTSTS-----TTSSSYSSSTSAFKD
79 PPRAPVILYDASEFKIHAHPNEMFALVORLTGPGSGPPAPPHQGEAQADYPMDEAAAQGFPELLLSPSAAMSPAAR
61 PGRAPVILYDASEFKIHAHPNEMFALVORLTGPGGAQQAHERHVADDDATAN--GGGVLGQAFLLPELLLSPSAAMSPAAR
52 QCRPVIYDASEFKIHTKPGIFMALVORLTGPGSTSAQAFDAAAAAGPS----HPAAMEFEPREFLLSPTAALSPAAR
33 THPKIKVRYISNPMRVETCPKREKRELVOELTG-----QDAADLPESPT
36 TNPKIKVRYISNPMRVETCPKREKRELVOELTG-----QDAADLPESPT
41 IKPKIRIHHIFAPEEIKTDVKNERSLVQSLTG-----KPE-TTKTGS
28 IKPKIRIHHIFAPEEIKTDVKNERSLVQSLTG-----KPE-TTKTGS
29 IKPKIRIHHIFAPEEIKTDVKNERSLVQSLTG-----KPE-TTKTGS
29 IKPKIRIHHIFAPEEIKTDVKNERSLVQSLTG-----KPE-TTKTGS
44 QLRPVIYITVSPKVIHATASEFMNVORLTG-----APPAPPPQOPH
40 GRASPVIYAHSPKVIHTRAEDFMALVORLTG-----LDEIRRNTESS
50 RRRPVIYITVSPKVIHATASEFMNVORLTG-----LDEIRRNTESS
35 GRRPIKVIYITVSPKVIHTRAEDFMALVORLTG-----LDEIRRNTESS
43 QRRPVIYITVSPKVIHTRAEDFMALVORLTG-----LDEIRRNTESS
8 -MTVPKIVITVNTQYLETDAASEFKSVORLTG-----NSTVEMVVAAPP
35 QTSPPKKKQRFSSNRDEHMMQMLDEGVOMGVPG-----ILLSDSSTLPP
      kr      pviy      SPkviht      efm      lVQrLTG      rpaavSP pr
      DOMAIN 2

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Figure 1B (2)

1C2 DELETION

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96 PAADQVAGGDHMAAAARADPTVLTG--QORQPPAPAPIDGDHPAAPPSPADA-----FLLSPSSFFLSPTTMMHALQ
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108 --LPSGTVSPAAATAEEGGGDPILLITGQORQ--AAAPAPPTITILLPSSAMAAAG-----MLLSPG--FLLSPSTMMQAIQ
94 YDAPAMVEQGATAACAGGDPILLITGQORQ--AASAPOPPAVPSF--MAAG-----MLLSPG--FVPSFNTMQSIQ
95 -----PPASSQQTACDILVLTGHHQH--VPPPPP--LPSF--GGAAG-----FLLSPG--FLLSPSTMMQAIQ
113 LAATENASPRGCKE-----PAARDEIVEINTAMEEAEFGGYAPGILSPSPAI-----LPTASTCTCFSMYHOGGM
114 LAATENASPRGCKEPV-----MAAKDEIVEIATAMEEAEFGGYAPGILSPSPAM-----LPTASAGCTFOMTHOGG
115 LAATENASPRGCKE-----EVESSTAMEEAEFGCYVPGILSPSPAM-----LPTVPAGCTFSFMFLHCGT
83 -----TTHVDFFNNGCGGMYSPARYATTEKAM-----SPMGCKHVLLSVNNIIS
108 ASTMVDTSFGLISPAERFAVTEKANTSNELCTFVGGECTMDQYYHYHHHHHHQ-----QOHQNGCFERFSFHAGT
159 LATHERSVRPMP-----EPAPPEYVDITNGGCGGVDGGAATLGSIRPGILSP--LPSSLEPAAVGQFSPLPFDASC
139 LATHERSVRPVP-----APAPADPYAADG-----HPRGCAAPREAPR--HPVPAAVLAAAGRRVGPVLAABAL
128 LATHERSVRPLPHHAPAAVPPYFGATNDCEFFLPGSADMDLSAALGPPACRPGILSPAALPPAATCTGTPMPFDPSC
76 TF-----TAVDLHRPCESEMNLEP-----LDGEVGEYYSPEDEEVFNAP--QM-----SAGLSGCFSSG
79 YS-----PSSDDHNLSPPAENLAPRVLHQEPFGERDSDCYEPTNAEDMTFEDQM-----SAGLSGCFSSNG
82 KK-----KITNTNFPAPPGLPQDSGOEHTAELDNRIIC--SHVKEEWGS-----SSNTNTYSDFDGIMDLID
72 KR-----AKSRITTPQEPVCDHQPVRNLSCTFTGLLANGGNHGVKEEWGSGDOS-----TSNTNTYSDLEGLIQDV
71 PR--RDMHRLHRQVQDMINTEKLREPEHCDQEFCLNAEETSMITWNNNGAGESS-----GGFLNGLDGFEFGIQEL
72 QKGLKRNPRSRSHDHHEVHDMNKSHGFCINSDEEEGCMYMTWNN--GDESS-----GGFLNGLDGIDGFIQEL
88 HPTLLAQMPPOPSFPFHLQQDAWPOQOHSAPAAEQAAARSAGDLEPLPSILSP--VPGTVLPAIPASFSPSPHISPV
85 SSVVTEEVNVEDNTAPFSQDRTORQKLDMPLETPPSMHLFGSPTQLMYMSP-----NRTDSRRELVEKSE
91 KFPFHFHFPSSVGAASRALLETSTSTSGVMSVTVVADTTCGGGSPVQOLPNHH-----MLVSSDPCDEPPPPSTCRVL
78 ASDDDDDGGCGGGGELAAASDGAGEPGPGTAASPDGTGAAASDADALVAAG-----HPAAATDDEGGGGGG
88 TSGVGGAGEAEPSEGERNKTRAAPPVRVKARALNRPVSVTTTRRQAAADASP-----PVDDLRLRYADEYRSNY
53 PTAANYRHCYINWDDQSSRALISETESTARKPSFSLGRGMSFNDFDNTEKEFP-----PSGLMLFQDLSPIRGAA
80 ISSNFSLVSLPSTPLYTFSPTETFSPTTSYIFSPKNNMLVPSNIDRKGTIPTQS-----EVYPMNMHQRILSKFLGG
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1C1 DELETION

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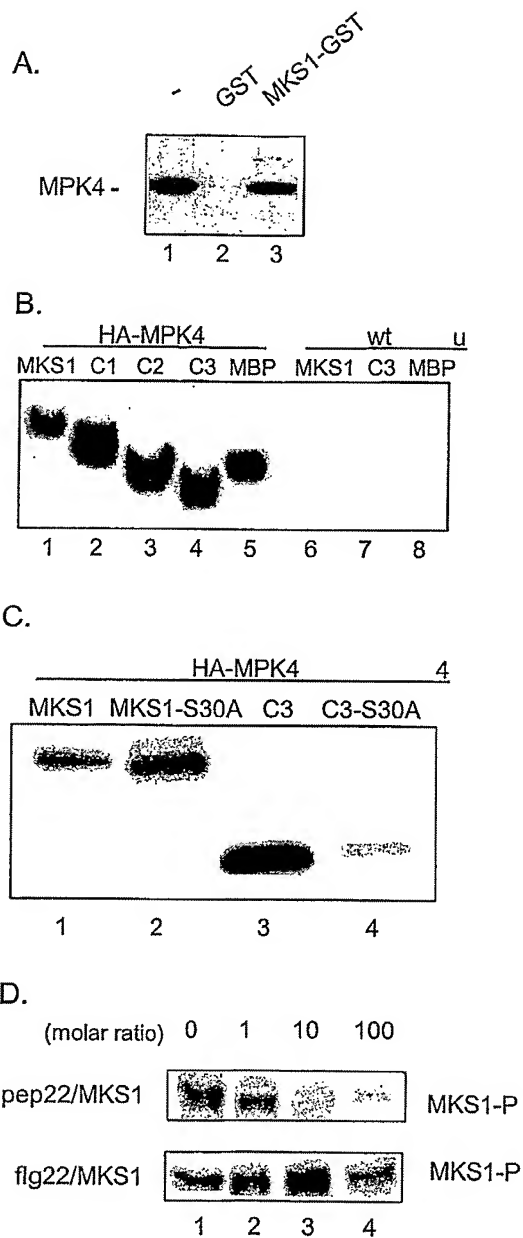
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177 ELNPLF-----c
162 ELSPLF-----d
152 EIIS-----e
179 FS-----PAIPLGLFSPAGFMSFPRSPGFT-----SLVASPTFADFFSHIWDQ-----f
182 MF-----SPG--LFSFAGLMSFPG--FA-----SLVASPTFADLFSHIWG-----g
175 FS-----PALPPGLFSPAGLMSPGYAS-----LASPNFADFFSHIWDP-----h
129 DV-----E-----i
180 LSPGFNSLPSVSPDFSTIGPTDPQGFSSFFNDFNSILQSSPSKIQSPSSMDLFNNFFDS-----j
231 ISWLNELSPILRAASAGAASSGGGSGGNTSNGGAARPPPSYADFPVPSRHLATPTVPSPATCAELFSLNPLD-----k
199 RPQORQLAQRAOPHPGSGVHGQRSAPLAHAHGPTGGSROP-----l
208 LSWLSELSPFLPSAGTRAAAAGLLDQAPFAPSRSLLSTPTMPS--PATFSVLEFFSSPNFPDL-----m
129 -----FYNVNALGSIGSL-----n
139 -----FYNVNDFGSIDSM-----o
142 -----EDDNIFSSRWFDLQQO-----p
138 GEDYFSSSFMRSSSSSQVEGFIFNNNNNNNNNNNNNNNTNFDTKAHNS-----q
140 G-----EFPYLPLSSIDASASSNSS-----r
141 G-----EFPYLPTTIDPAVASSSHLGNVFAEPHYA-----s
166 PFLGATTSSAAPSTSPSPMGGSAYYWDLFNMQQQHYHHQN-----t
-----u
165 SSNTTAVVSSSTNTSKNYE-----v
148 GYDDDDDDIFRSQLLDTSYSVFSPTLLYDHPHKS-----w
159 LKGEHLPLVSPAWLHVGDHFLSPAGAAAALGSPSPSFVDDIFGTLSSQQO-----x
125 -----y
156 AKPP-----z

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f: MKS1 At3g18690 f: BoBH544707 g: BoBOHT92TR + BOGQI24TF h: GmBE020960
i: At1g21326 j: OsCAD40925 k: ZmCC613160 l: ZmCC635639 m: At2g41180
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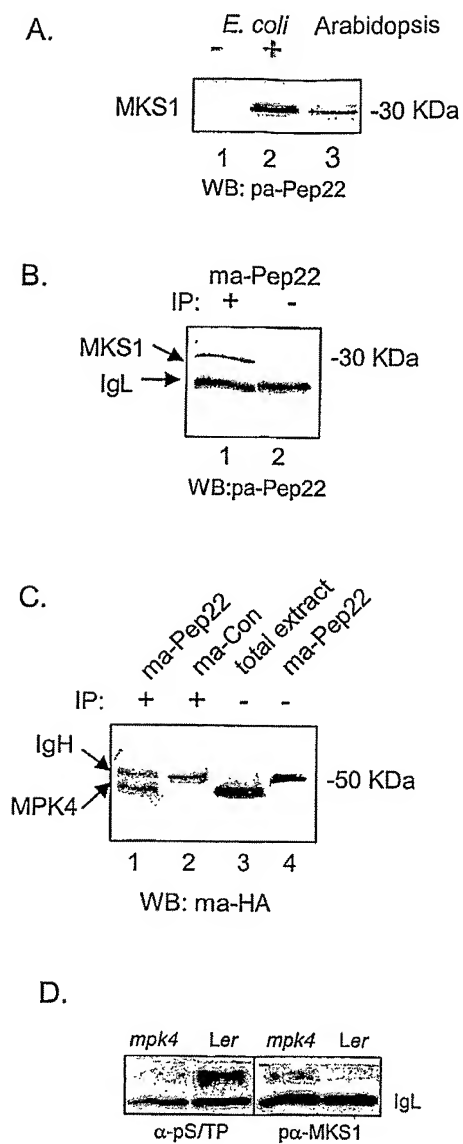
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Figure 2.



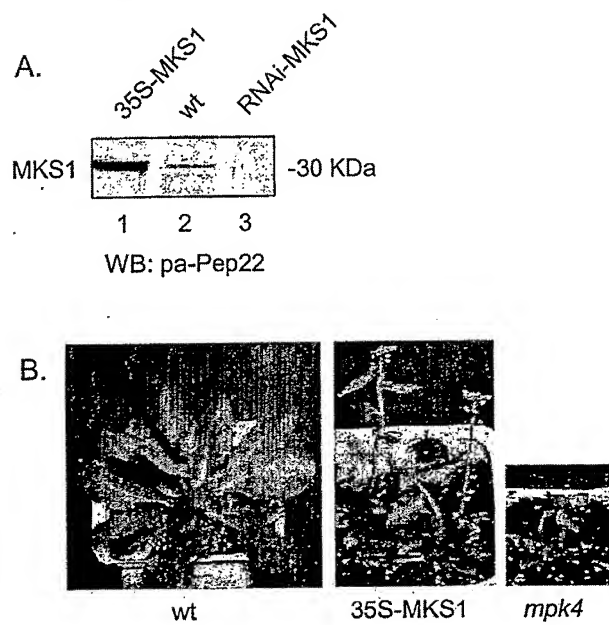
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Figure 3.



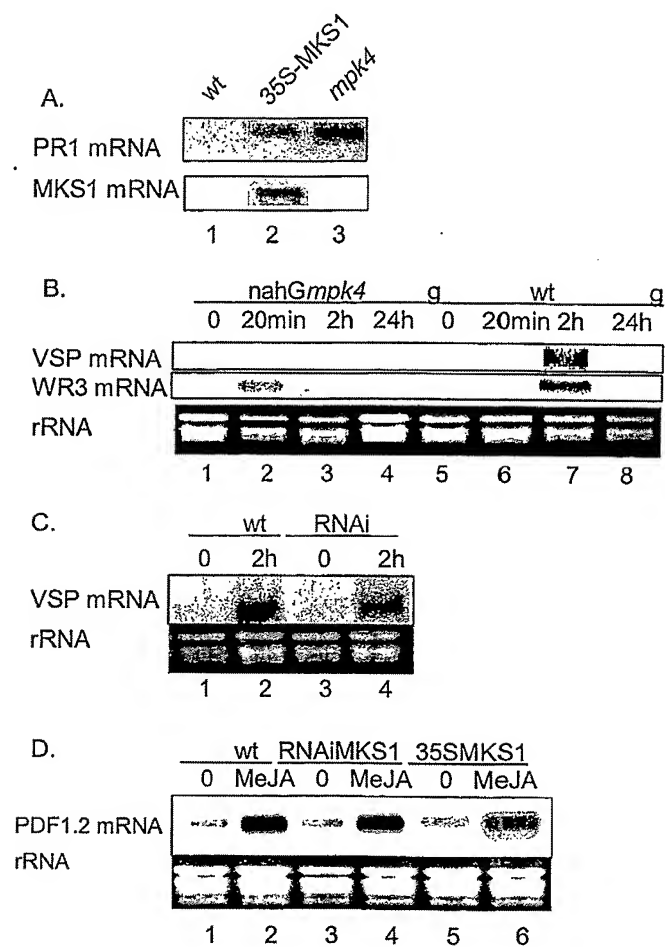
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Figure 4.



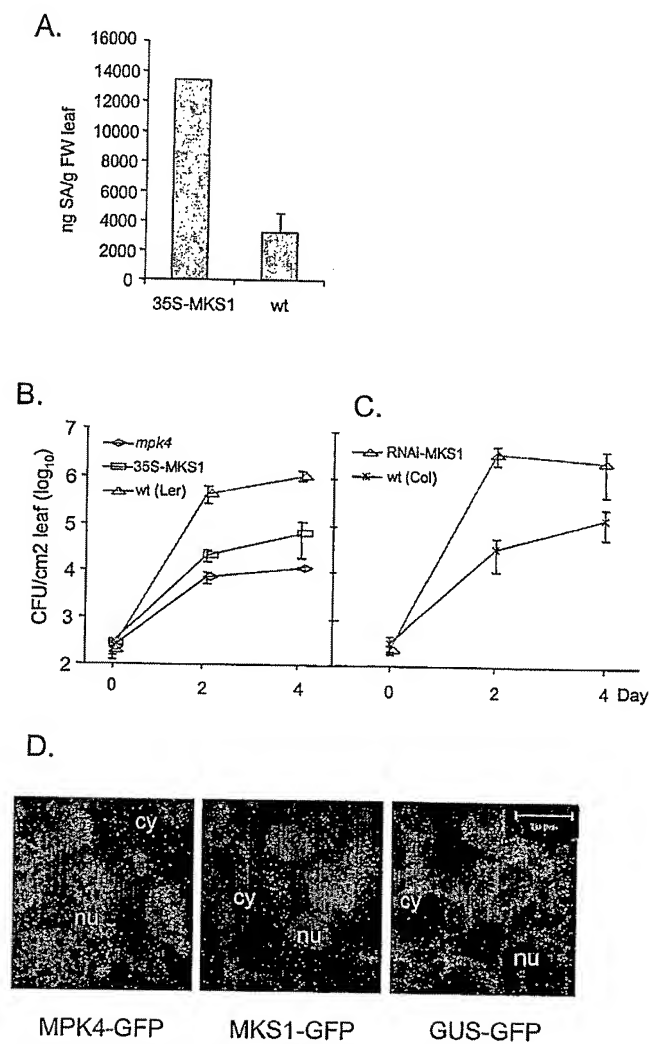
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Figure 5.



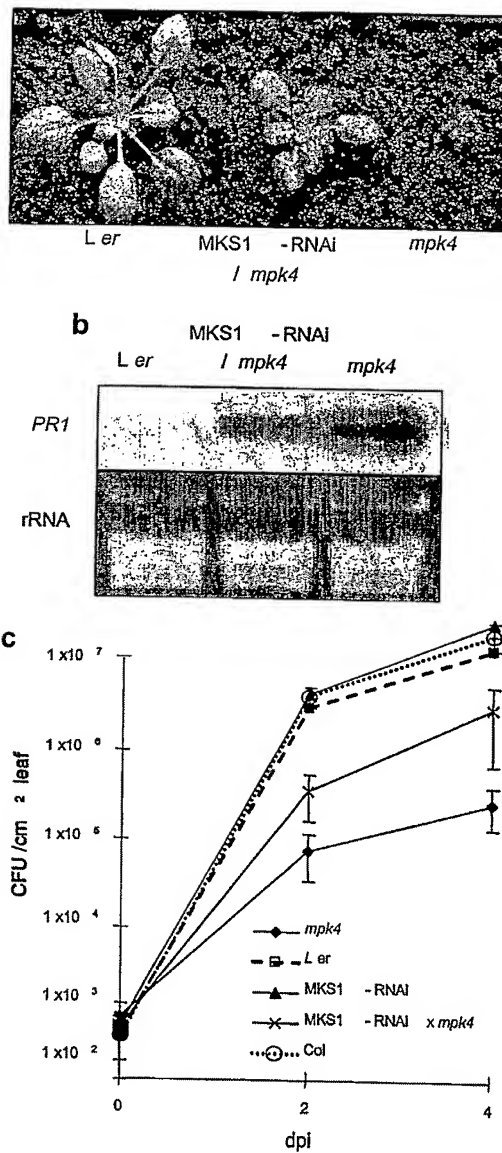
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Figure 6.



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Figure 7



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Figure 8.

